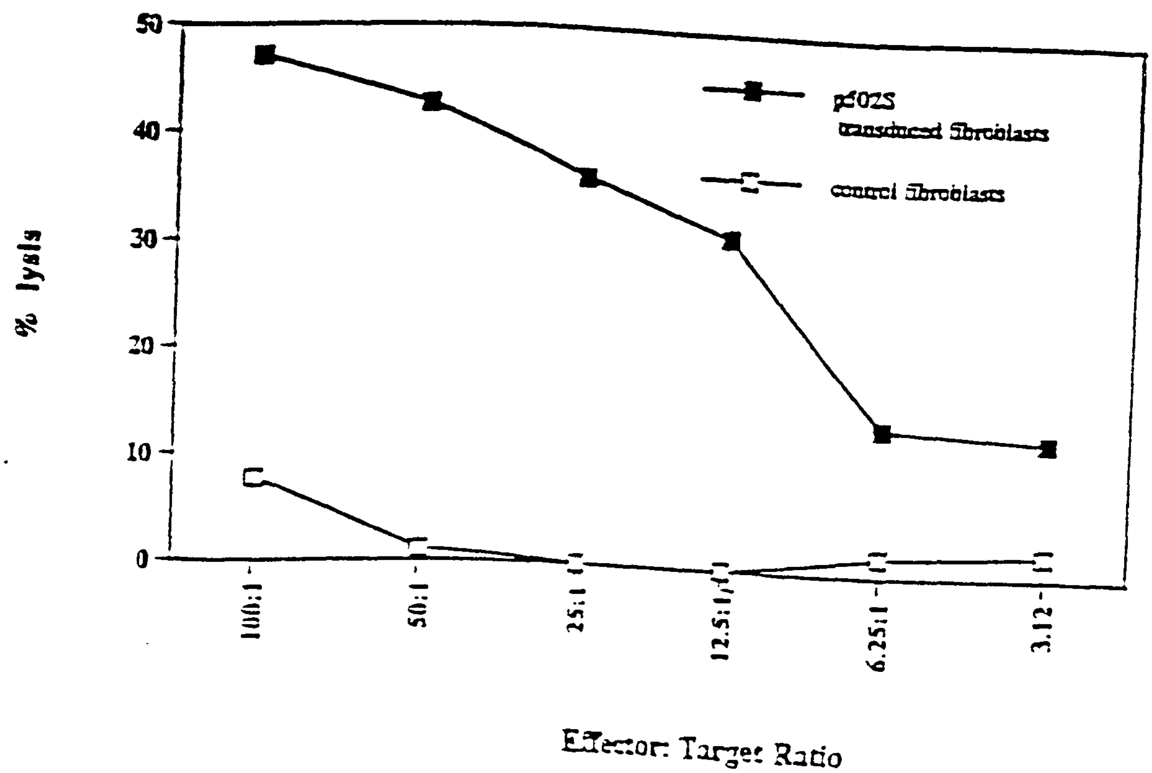
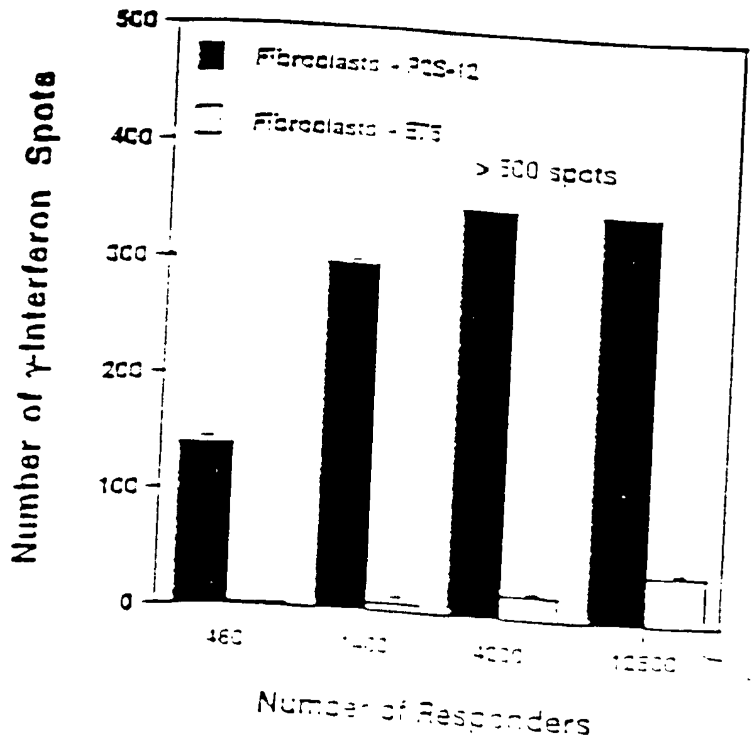

50
40
30
20
10
0
% lysis
p502S
transduced fibroblasts
control fibroblasts
100:1
50:1
25:1
12.5:1
6.25:1
3.12
Effector: Target Ratio

Fig. 1



Number of γ-Interferon Spots
500
400
300
200
100
0
> 300 spots
Number of Responders

Fig. 2A

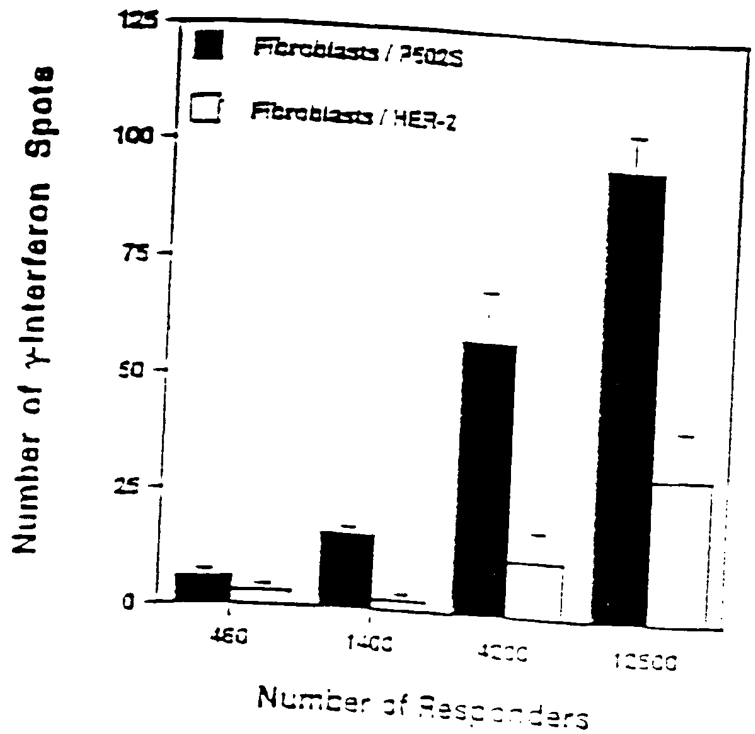

Fibroblasts / P502S
Fibroblasts / HER-2
Number of γ-Interferon Spots
125
100
75
50
25
0
460
1400
4000
12500
Number of Responders

Fig. 2B

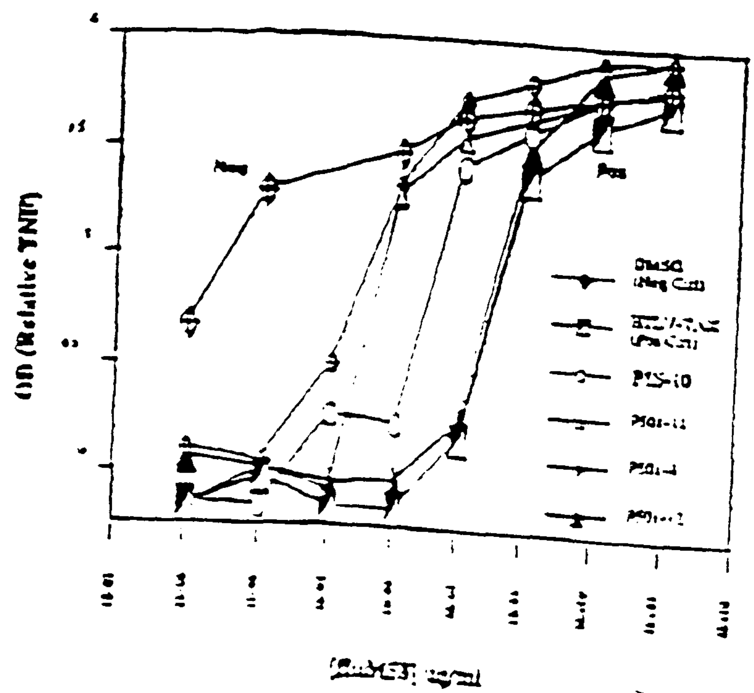
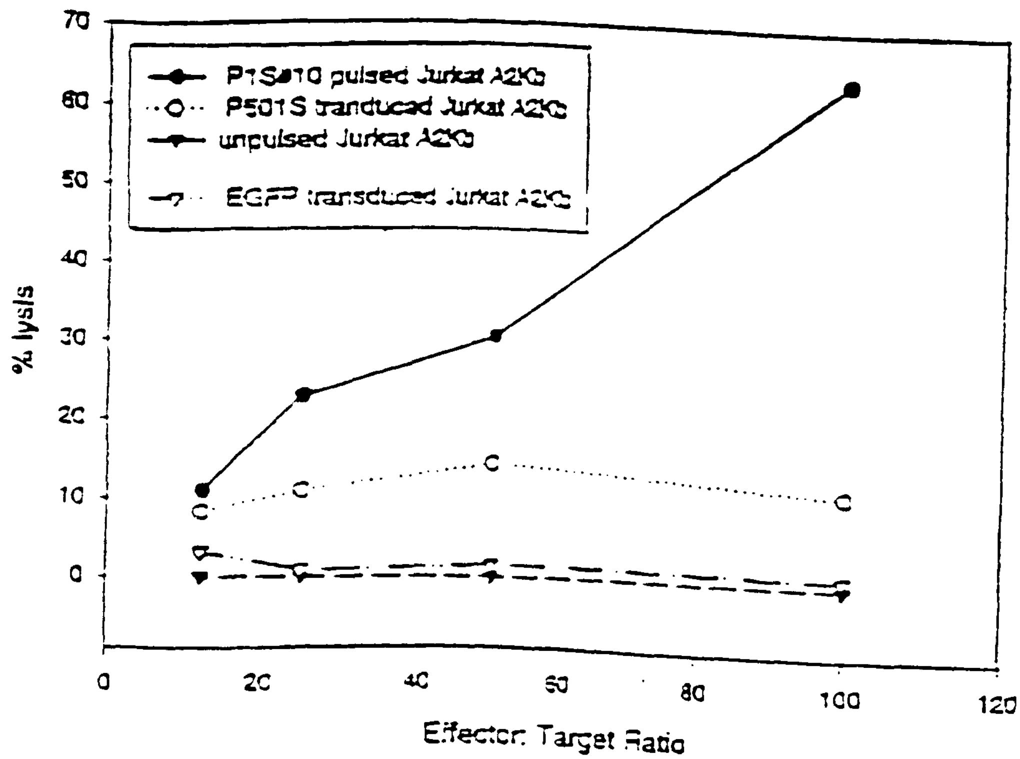


Fig. 3



70
60
50
40
30
20
10
0
% lysis
P1S#10 pulsed Jurkat A2Kb
P501S tranducad Jurkat A2Kb
unpulsed Jurkat A2Kb
EGFP transduced Jurkat A2Kb
0
20
40
60
80
100
120
Effector: Target Ratio

Fig. 4

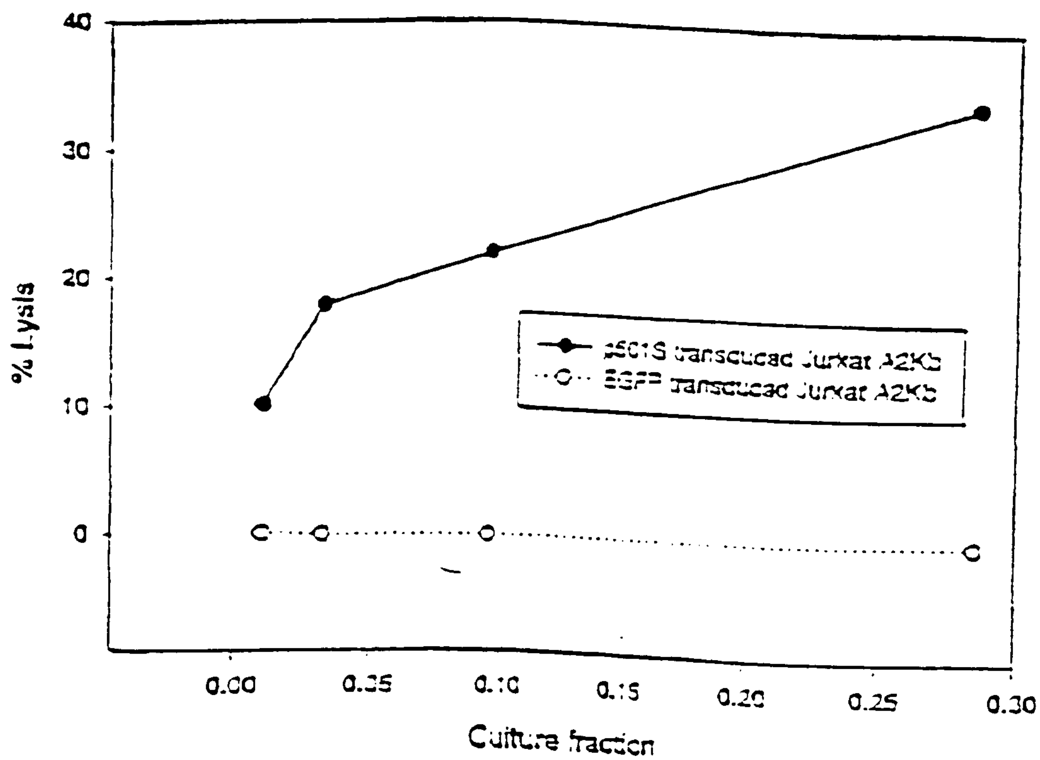


Fig. 5

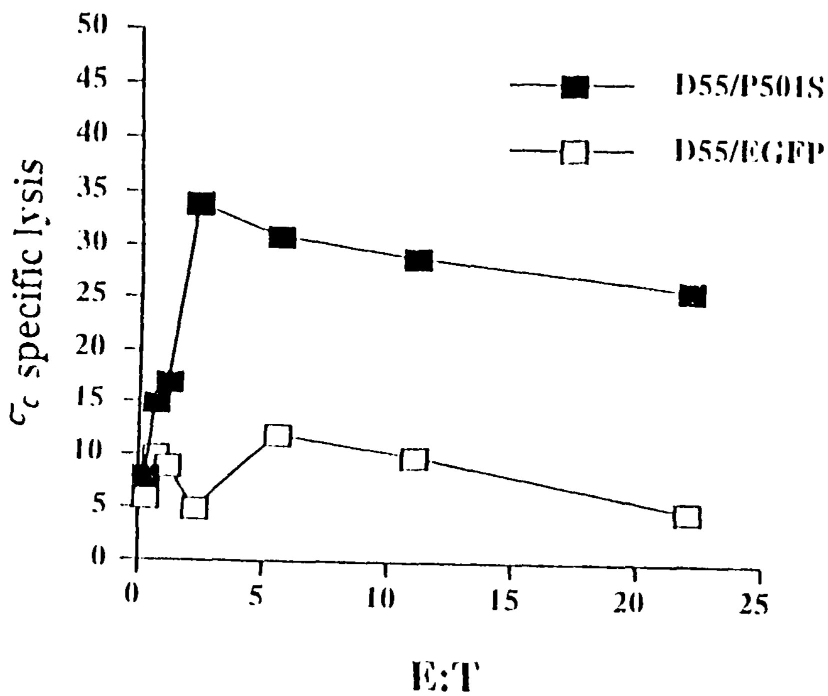

% specific lysis
50
45
40
35
30
25
20
15
10
5
0
0
5
10
15
20
25
E:T
D55/P501S
D55/EGFP

Fig. 6A

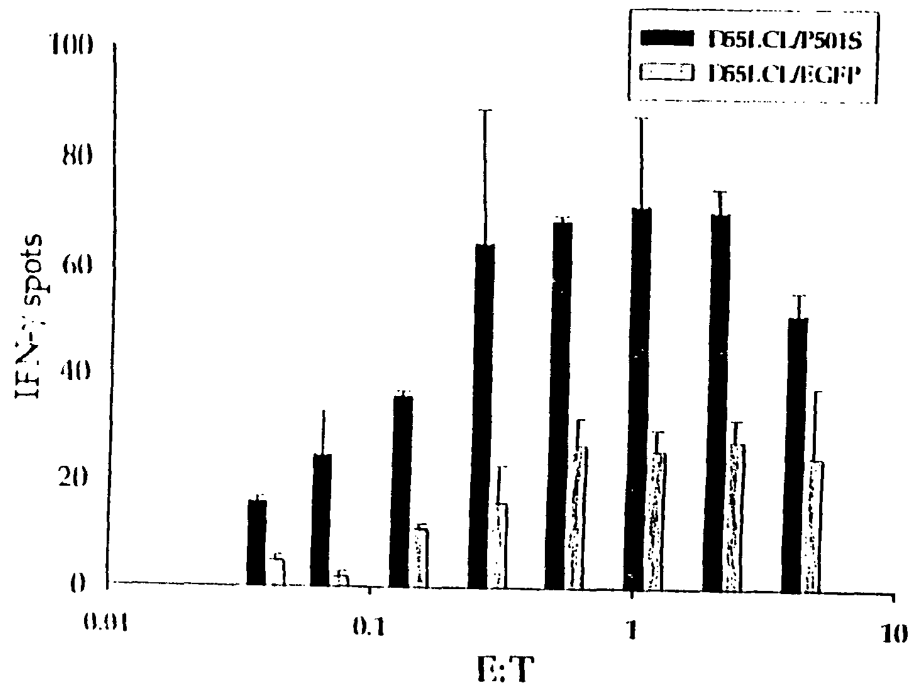
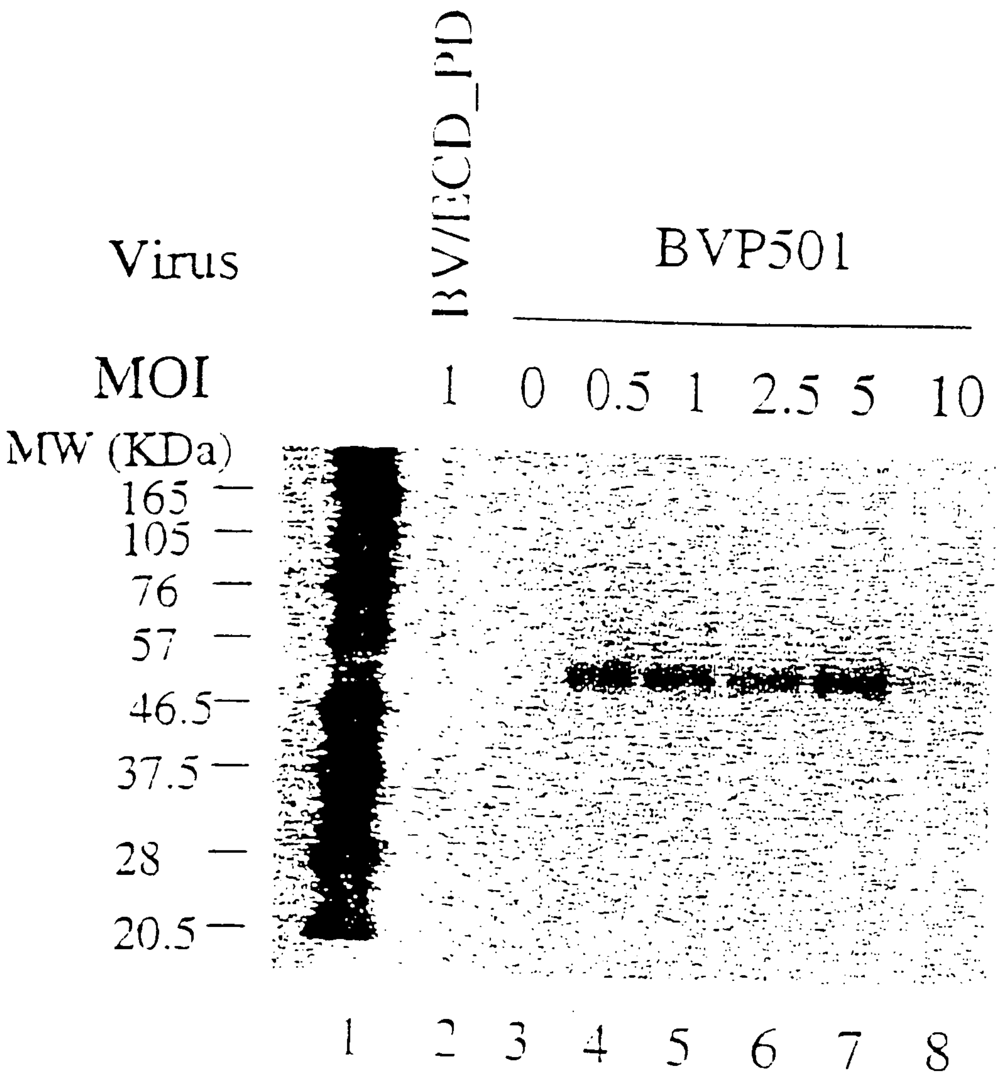

IFN-γ spots
100
80
60
40
20
0
0.01
0.1
1
10
E:T
D651.CL/P501S
D651.CL/EGFP

Fig. 6B

Expression of P501S
by the Baculovirus Expression System



0.6 million high 5 cells in 6-well plate were infected with an unrelated control virus BV/ECD_PD (lane 2), without virus (lane 3), or with recombinant baculovirus for P501 at different MOIs (lane 4 - 8). Cell lysates were run on SDS-PAGE under the reducing conditions and analyzed by Western blot with a monoclonal antibody against P501S (P501S-10E3-G4D3). Lane 1 is the biotinylated protein molecular weight marker ([illegible]Labs).

Fig. 7

Figure 8. Mapping of the epitope recognized by 10E3-G4-D3

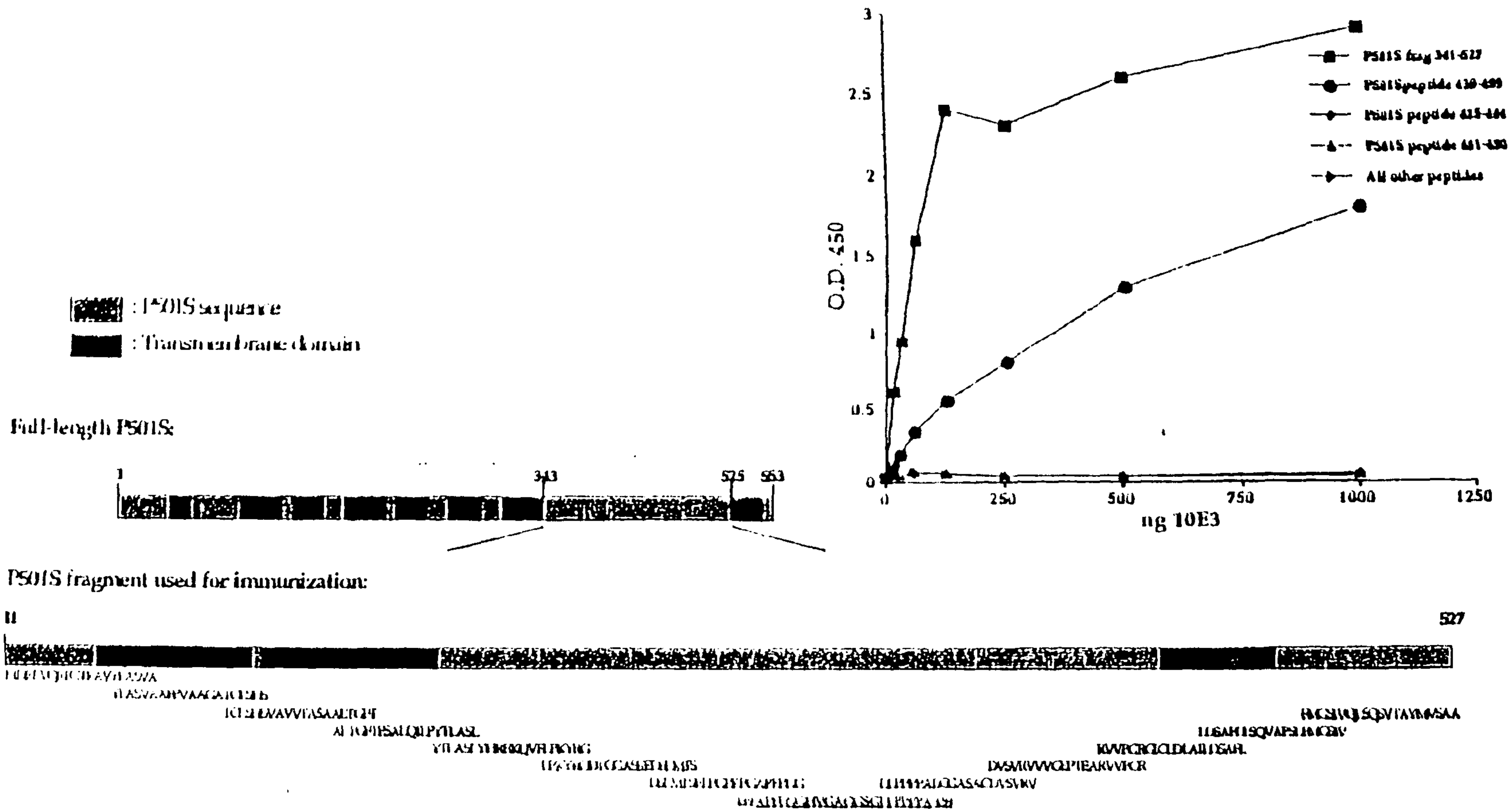


Fig. 8

0011770"22528160

Figure 1. Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT **YVPPLLLEVGVEEKFM** TMVLGIGPVLGLVCVPLLGSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL AGLLCPDPRPLE LALLILGVGLLDFCGQVCFTPL

EALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI **DWDTSALAPYLGTQEE**

CLFGLLTLIFLTCVAATLLV *AEEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL*

HQLCCRMPRTLRR LFVAELCSWMALMTFTLFYTDF VGEGLYQGVP**RAEPGTEARRHYDEGVR**

MGSLGLFLQCAISLVFSLVM *DRLVQRFGTRAVYLAS* VAAFPVAAGATCLSHSVAVVTA **SAA**

LTGFTFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL*

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF **MGSIVQLSQS**

VTAYMVSAAGLGLVAIYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; **Bold sequence**: Predicted extracellular domain; *Italic sequence*: Predicted intracellular domain. Sequence in bold/underlined: used to generate polyclonal rabbit serum

Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon (1998) Principles Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology Prediction. J.Mol Biol. 283, 489-506.

Fig. 9

Genomic Map of (5) Corixa Candidate Genes

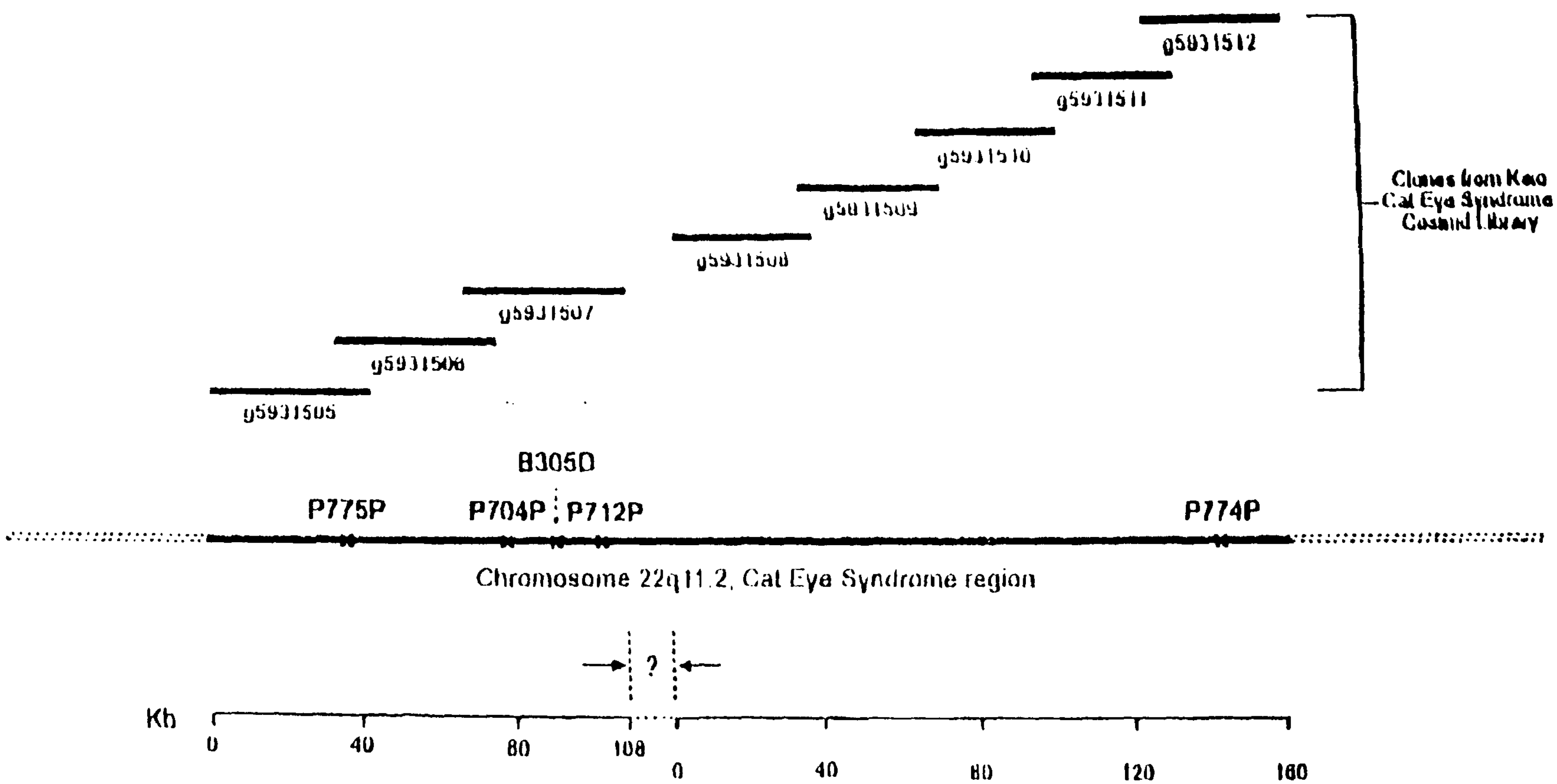


Fig. 10

FIGURE 4. Elisa assay of rabbit polyclonal antibody specificity

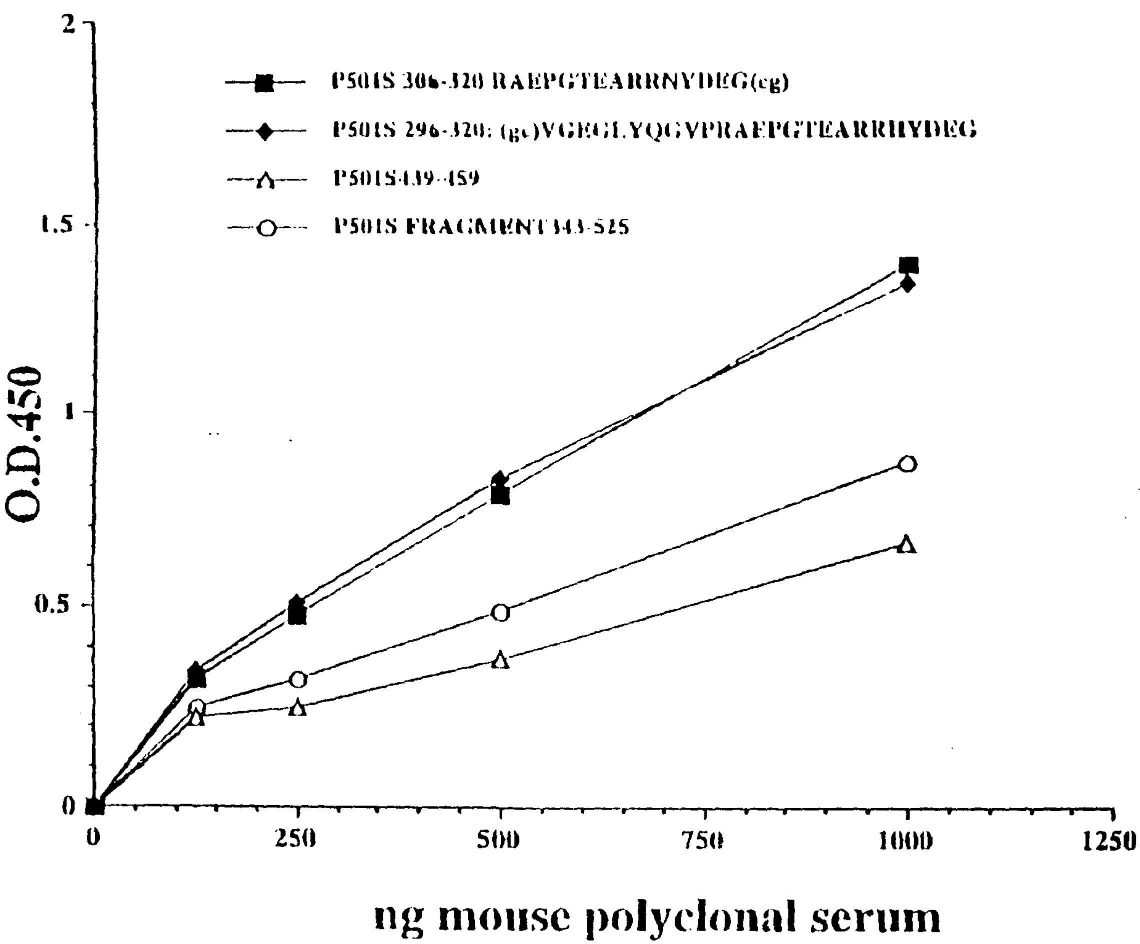


Fig. 11

```
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GAATTTTATTCAAGCAAATTTTAAGAAACGAGAATGTGTCTTCTTTACCAAAGATTCCAAGGCCACGGAG 210
AATGTGTGCAAGTGTGGCTATGCCCAGAGCCAGCACATGGAAGGCACCCAGATCAACCAAAGTGAGAAAT 280
GGAACTACAAGAAACACACCAAGGAATTTCCTACCGACGCCTTTGGGGATATTCAGTTTGAGACACTGGG 350
       360       370       380       390       400       410       420
GAAGAAAGGGAAGTATATACGTCTGTCCTGCGACACGGACGCGGAAATCCTTTACGAGCTGCTGACCCAG 420
CACTGGCACCTGAAAACACCCAACCTGGTCATTTCTGTGACCGGGGGCGCCAAGAACTTCGCCCTGAAGC 490
CGCGCATGCGCAAGATCTTCAGCCGGCTCATCTACATCGCGCAGTCCAAAGGTGCTTGGATTCTCACGGG 560
AGGCACCCATTATGGCCTGACGAAGTACATCGGGGAGGTGGTGAGAGATAACACCATCAGCAGGAGTTCA 630
GAGGAGAATATTGTGGCCATTGGCATAGCAGCTTGGGGCATGGTCTCCAACCGGGACACCCTCATCAGGA 700
       710       720       730       740       750       760       770
ATTGCGATGCTGAGGGCTATTTTTTAGCCCAGTACCTTATGGATGACTTCACAAGGGATCCACTGTATAT 770
CCTGGACAACAACCACACACATTTGCTGCTCGTGGACAATGGCTGTCATGGACATCCCACTGTCGAAGCA 840
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TAAAATTCCTTGTGTGGTGGTGGAAGGCTCGGGCCGGATCGCTGATGTGATCGCTAGCCTGGTGGAGGTG 1050
      1060      1070      1080      1090      1100      1110      1120
GAGGATGCCCCGACATCTTCTGCCGTCAAGGAGAAGCTGGTGCGCTTTTTACCCCGCACGGTGTCCCGGC 1120
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TTCAGCACCAGTGAGCAAGACAAGGATAACTGGAATGGGCAGCTGAAGCTTCTGCTGGAGTGGAACCAGC 1330
TGGACTTAGCCAATGATGAGATTTTCACCAATGACCGCCGATGGGAGTCTGCTGACCTTCAAGAAGTCAT 1400
      1410      1420      1430      1440      1450      1460      1470
GTTTACGGCTCTCATAAAGGACAGACCCAAGTTTGTCCGCCTCTTTCTGGAGAATGGCTTGAACCTACGG 1470
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AAGAGGCTTCCGGAAGGAAGACAGAAATGGCCGGGACGAGATGGACATAGAACTCCACGACGTGTCTCCT 1680
ATTACTCGGCACCCCCTGCAAGCTCTCTTCATCTGGGCCATTCTTCAGAATAAGAAGGAACTCTCCAAAG 1750
      1760      1770      1780      1790      1800      1810      1820
TCATTTGGGAGCAGACCAGGGGCTGCACTCTGGCAGCCCTGCGAGCCAGCAAGCTTCTGAAGACTCTGGC 1820
CAAAGTGAAGAACGACATCAATGCTGCTGGGGAGTCCGAGGAGCTGGCTAATGAGTACGAGACCCGGGCT 1890
GTTGAGCTGTTCACTGAGTGTTACAGCAGCGATGAAGACTTGGCAGAACAGCTGCTGGTCTATTCCTGTG 1960
AAGCTTGGGGTGGAAGCAACTGTCTGGAGCTGGCGGTGGAGGCCACAGACCAGCATTTCACCGCCCAGCC 2030
TGGGGTCCAGAATTTTCTTTCTAAGCAATGGTATGGAGAGATTTCCCGAGACACCAAGAACTGGAAGATT 2100
```

Fig. 12A

2110 2120 2130 2140 2150 2160 2170

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AGCACAAGAAGCTGCTTTGGTACTATGTGGCGTTCTTCACCTCCCCCTTCGTGGTCTTCTCCTGGAATGT 2240
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CCCCCCGAGCTGCTCCTGTACTCCCTGGTCTTTGTCCTCTTCTGTGATGAAGTGAGACAGTGGTACGTAA 2380
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2460 2470 2480 2490 2500 2510 2520

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TGCTGCAGAGGATGCTGATCGATGTGTTCTTCTTCCTGTTCCTCTTTGCGGTGTGGATGGTGGCCTTTGG 2660
CGTGGCCAGGCAAGGGATCCTTAGGCAGAATGAGCAGCGCTGGAGGTGGATATTCCGTTCGGTCATCTAC 2730
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2810 2820 2830 2840 2850 2860 2870

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GTCGCCATGTTTGGCTACACGGTGGGCACCGTCCAGGAGAACAATGACCAGGTCTGGAAGTTCCAGAGGT 3010
ACTTCCTGGTGCAGGAGTACTGCAGCCGCCTCAATATCCCCTTCCCCTTCATCGTCTTCGCTTACTTCTA 3080
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3160 3170 3180 3190 3200 3210 3220

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CAAGGGTCTTCTGAAAGAGATTGCTAATAAAATCAAATAAAACTGTATGAAACTCTAATGGAGAAAAATC 3360
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3510 3520 3530 3540 3550 3560 3570

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GCCTGTTTCTCTCTGTGTCTCAATGCCTGGGACTGGAGGTTGATAGTTTAAGTGTGTTCTTACCGCCTCC 3640
TTTTTCCTTTAATCTTATTTTGATGAACACATATATAGGAGAACATCTATCCTATGAATAAGAACCTGG 3710
TCATGCTTTACTCCTGTATTGTTATTTTGTTCATTTCCAATTGATTCTCTACTTTTCCCTTTTTTGTATT 3780
ATGTGACTAATTAGTTGGCATATTGTTAAAAGTCTCTCAAATTAGGCCAGATTCTAAAACATGCTGCAGC 3850

3860 3870 3880 3890 3900 3910 3920

AAGAGGACCCCGCTCTCTTCAGGAAAAGTGTTTTCATTTCTCAGGATGCTTCTTACCTGTCAGAGGAGGT 3920
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4210 4220 4230 4240 4250 4260 4270

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4560 4570 4580 4590 4600 4610 4620

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4910 4920 4930 4940 4950 4960 4970

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5260 5270 5280 5290 5300 5310 5320

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5610 5620 5630 5640 5650 5660 5670

GTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5668

10 20 30 40 50 60 70

MRNRRNDTLDSTRTLYSSASRSTDLSYSESDLVNFIQANFKKRECVFFTKDSKATENVCKCGYAQSQHME 70
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GGAKNFALKPRMRKIFSRLIYIAQSKGAWILTGGTHYGLTKYIGEVVRDNTISRSSEENIVAIGIAAWGM 210
VSNRDTLIRNCDAEGYFLAQYLMDDFTRDPLYILDNNHTHLLLVDNGCHGHPTVEAKLRNQLEKHISERT 280
IQDSNYGGKIPIVCFAQGGGKETLKAINTSIKNKIPCVVVEGSGRIADVIASLVEVEDAPTSSAVKEKLV 350

360 370 380 390 400 410 420

RFLPRTVSRLSEEETESWIKWLKEILECSHLLTVIKMEEAGDEIVSNAISYALYKAFSTSEQDKDNWNGQ 420
LKLLLEWNQLDLANDEIFTNDRRWESADLQEVMFTALIKDRPKFVRLFLENGLNLRKFLTHDVLTELFSN 490
HFSTLVYRNLQIAKNSYNDALLTFVWKLVANFRRGFRKEDRNGRDEMDIELHDVSPITRHPLQALFIWAI 560
LQNKKELSKVIWEQTRGCTLAALGASKLLKTLAKVKNDINAAGESEELANEYETRAVELFTECYSSDEDL 630
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710 720 730 740 750 760 770

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1060 1070 1080 1090 1100 1110 1120

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Fig. 12B